K123891

# 510(k) Summary


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**Device Trade Name:** **Spartan RX™ CYP2C19 System**
*For the assay:* Spartan RX CYP2C19 Assay
*For the platform:* Spartan RX CYP2C19 Platform

**Device Common Name:** Drug metabolizing enzyme genotyping assay

**Measurand:** CYP450 2C19 *2, *3, *17

**Sample Type:** DNA from buccal cells

**Technology:** Polymerase Chain Reaction (PCR)

**Device Panel:** Chemistry and Toxicology

**Classification Name:** Drug metabolizing enzyme genotyping system, 862.3360
Instrumentation for clinical multiplex test systems, 862.2570

**Classification Code:** NTI: Drug metabolizing enzyme genotyping system
NSU: Instrumentation for clinical multiplex test systems

**Predicate Device:** INFINITI CYP2C19 Assay, 510(k) Number K101683
Classification Code: NTI and NSU, Regulation No. 862.3360 and 862.2570

**Intended Use**

The Spartan RX CYP2C19 System is a qualitative *in vitro* diagnostic test for the identification of a patient's CYP2C19 *2, *3 and *17 genotype determined from genomic DNA obtained from a buccal swab sample. For prescription use only.

**Indication for Use**

**Spartan RX CYP2C19 Assay -** The Spartan RX CYP2C19 System is indicated for use as an aid to clinicians in determining therapeutic strategies for therapeutics that are metabolized by the Cytochrome P450 2C19 gene product, and that are specifically affected by the *2, *3, and *17 alleles. The Spartan RX CYP2C19 Assay will be run on the Spartan RX CYP2C19 Platform from the buccal sample collected with

a buccal swab. The Spartan RX CYP2C19 Assay is not indicated to be used to predict drug response or non-response.

**Spartan RX CYP2C19 Platform -** The Spartan RX CYP2C19 System is indicated for use as an aid to clinicians in determining therapeutic strategies for therapeutics that are metabolized by the Cytochrome P450 2C19 gene product, and that are specifically affected by the *2, *3, and *17 alleles. The Spartan RX CYP2C19 Platform will be used to run the Spartan RX CYP2C19 Assay.

**Device Description**

The Spartan RX CYP2C19 System is a sample-to-result DNA testing system that uses proprietary technology to integrate DNA extraction and amplification. Genotypes are determined using PCR and fluorescent probe detection. The Spartan RX CYP2C19 System is comprised of the Spartan RX CYP2C19 Platform and Spartan RX CYP2C19 Assays. The Spartan RX CYP2C19 Assays are run on the Spartan RX CYP2C19 Platform.

The Spartan RX CYP2C19 System is based on the following processes:

i. Buccal swab collection
ii. DNA extraction
iii. PCR-based amplification of the target gene
iv. Detection of the *2, *3, and *17 alleles using fluorescent-probes
v. Fluorescent signal detection and analysis
vi. Genotype determination

The Spartan RX CYP2C19 System integrates and automates steps ii to vi. Results are presented to the end user as genotype calls. The system also has integrated controls that monitor performance of a run and automatically inform the user of any anomalies in the instrument or reagents.

The system detects the CYP2C19 *2, *3, and *17 genotypes in separate reagent tubes. The operator collects buccal swab samples from a patient; inserts each sample into a reagent tube; and then inserts the reagent tubes into a Spartan RX Analyzer instrument.

***Spartan RX CYP2C19 Platform***

There are four components of the Spartan RX CYP2C19 Platform.

a) The SPARTAN RX ANALYZER is a thermal cycling instrument that automates polymerase chain reaction (PCR) amplification of the target gene, fluorescence-based detection of CYP2C19 alleles, and genotype calling.

b) The NETBOOK serves as the user interface for logging in to the Spartan RX Platform, inputting patient information, and starting a test.

c) The PRINTER automatically prints the genotype results after the Spartan RX Platform finishes performing the Spartan RX CYP2C19 Assays.

d) The BARCODE SCANNER is used to automatically enter SCK and ECK lot numbers into the Spartan RX Platform.

***Spartan RX CYP2C19 Assays***

The Spartan RX CYP2C19 Assays are the consumable components of the Spartan RX CYP2C19 System. There are two different types of assay—each type is described in detail below.

a) SAMPLE COLLECTION KITS (SCKs) contain the consumables required to determine a patient's CYP2C19*2, *3, or *17 genotype. There are three types of SCKs, specific for the *2, *3, or *17 alleles. Each SCK consists of the following components:

- POUCH, containing labeling information to ensure traceability (lot number, manufacturing date, and expiry date) and two compartments (for the buccal swab and reagent tube). The pouch also includes a barcode that is compatible with a standard reader.
- BUCCAL SWAB, used to collect a buccal sample from the inside of a patient's cheek and transfer it into the reagent tube.
- REAGENT TUBE, containing chemicals for DNA extraction, PCR amplification, and fluorescent detection of the specific CYP2C19 allele.

The SCKs are color-coded to indicate which CYP2C19 allele they are designed to detect.
- BLUE = *2
- WHITE = *3
- BLACK = *17

b) EXTERNAL CONTROL KITS (ECKs) contain the consumables required to determine if the Spartan RX Platform and reagents are performing correctly. Each ECK consists of the following components:
- POUCH, containing labeling information to ensure traceability (lot number, manufacturing date, and expiry date).
- REAGENT TUBE, containing synthetic nucleic acid control and chemicals for PCR amplification and fluorescent detection of the specific CYP2C19 allele.

The ECKs are color-coded to indicate which reagent they control for.
- BLUE = *2
- WHITE = *3
- BLACK = *17

The ECKs have been modified so that the tube cannot be opened. They are meant to be put directly into the analyzer without adding or removing anything from them

***Spartan RX Accessories***

The SAMPLE TRANSPORT SYSTEM is an insulated transport bag that contains a polystyrene box and a Cold Block. The Transport System is designed to keep the SCKs cold as they are moved from the freezer to the patient and from the patient to the Spartan RX Analyzer. The Transport System is provided with purchase of the platform and is to be used for all tests..

**Substantial Equivalence Discussion**

The Spartan RX CYP2C19 System uses the same fundamental scientific technologies, and has a similar intended use, as that of the predicate device—the INFINITI CYP2C19 Assay. The table below provides a comparison of the Spartan RX CYP2C19 System and the predicate device. The comparison demonstrates that the Spartan RX CYP2C19 System is substantially equivalent to the predicate device.

**Table 1 – Comparison of the Spartan RX CYP2C19 System to the predicate device**

| **Characteristic** | **Predicate Device INFINITI CYP2C19 Assay (K101683)** | **Subject Device Spartan RX CYP2C19 System** |
|---|---|---|
| | **Similarities** | |
| Intended Use | The INFINITI CYP2CI9 Assay is an in vitro diagnostic test for the identification of a patient's CYP450 2C19 genotype in genomic deoxyribonucleic acid (DNA) obtained **from EDTA-anticoagulated whole blood samples.** The INFINITI CYP2CI9 | The Spartan RX CYP2C19 System is a qualitative *in vitro* diagnostic test for the identification of a patient's CYP2C19 *2, *3 and *17 genotype determined from genomic DNA obtained **from a buccal swab sample.** For prescription use only. |

| Characteristic | Predicate Device<br>INFINITI CYP2C19 Assay<br>(K101683) | Subject Device<br>Spartan RX CYP2C19 System |
|---|---|---|
| | Assay is a qualitative<br>assay for use in clinical laboratories upon prescription by the attending physician. | |
| Indication for Use | The INFINITI CYP2C19 Assay is indicated for use as an aid to clinicians in determining<br>therapeutic strategy for therapeutics that are metabolized by the CYP450 2CI9 gene product,<br>specifically *2, *3, * 17.<br><br>The INFINITI CYP2CI9 Assay is not indicated to be used to predict drug response or nonresponse. | Spartan RX CYP2C19 Assay - The Spartan RX CYP2C19 System is indicated for use as an aid to clinicians in determining therapeutic strategies for therapeutics that are metabolized by the Cytochrome P450 2C19 gene product, and that are specifically affected by the *2, *3, and *17 alleles. **The Spartan RX CYP2C19 Assay will be run on the Spartan RX CYP2C19 Platform from the buccal sample collected with a buccal swab.** The Spartan RX CYP2C19 Assay is not indicated to be used to predict drug response or non-response.<br><br>Spartan RX CYP2C19 Platform - The Spartan RX CYP2C19 System is indicated for use as an aid to clinicians in determining therapeutic strategies for therapeutics that are metabolized by the Cytochrome P450 2C19 gene product, and that are specifically affected by the *2, *3, and *17 alleles. The Spartan RX CYP2C19 Platform will be used to run the Spartan RX CYP2C19 Assay. |
| Limitations | Not intended to be used to predict drug response or non-response. | Same |
| DNA Sequence | Detects specific DNA sequences through recognition of DNA targets with fluorescence. | Same |
| Technology | Utilizes thermal cycling and target DNA amplification. | Same |
| Assay Results | Assay signal results are interpreted by a software program.<br>Assay results are provided as genotype calls reported to the end user in a report format. | Same |
| Target Gene | CYP4502C19 *2, *3, and *17. | Same |
| | **Differences** | |
| Specimen Type | Purified DNA from EDTA-anti-coagulated whole blood sample. | Unpurified DNA from a buccal swab sample. |
| Platform | Microarray-based genotyping test for simultaneous (multiplex system) of DNA sequences. | Fluorescent-probe PCR-based genotyping test for multiplex analysis of DNA sequences. |
| | **Trial Calling Rates** | |
| Reproducibility (% agreement/ 95% Lower CI) | 96.9% / 95.6% | 99.8% / 99.4% |
| Method comparison (% agreement/ 95% Lower CI) | 100.0% / 99.8% | 100.0% / 99.2% |

## Performance

### *Limit of Detection (Analytical Sensitivity)*

The input material for the Spartan RX CYP2C19 System is a buccal swab collected from an individual, which is inserted directly into the reagent tube without any requirement for the user to extract or purify DNA. For this reason, the objective of the limit of detection (LOD) study was to determine if the Spartan RX CYP2C19 System can function across the range of target material amounts collected in typical buccal swabs. The study was conducted in two parts.

Part 1 involved the determination of a relative measure of the amount of DNA present in 100 individual buccal swabs, collected from 40 different individuals by 11 different operators. These operators had laboratory- and non-laboratory backgrounds. The mean DNA amount was deemed to be equivalent to one "typical" swab and all measurements were normalized to this value and presented as the number of swab equivalents.

Part 2 assessed the analytical sensitivity (limit of detection) by analyzing buccal swab samples collected from *1/*1, *2/*17, *17/*17, and *2/*3 individuals. Five DNA collection conditions were used: 5 pooled buccal swabs; 2 pooled buccal swabs; a normal buccal swab; a single downward stroke (1 half stroke); and a single touch of the swab to the inside of the mouth. Replicates of 52 samples were performed for each condition. Results are summarized in Tables 2a and 2b. In parallel, the amount of DNA in the swabs was quantified using SYBR Green (standard curve), and this value was translated to the corresponding number of swabs relative to the mean of the population determined in Part 1.

**Table 2a – Limit of Detection – FIRST PASS**

| Test Condition | Genotype[a] | # Samples tested | # Correct calls[b] | # Incorrect calls | # No calls | % Correct calls | 95% One-sided confidence lower limit) |
|---|---|---|---|---|---|---|---|
| 5 pooled swabs | *1/*1 | 13 | 11 | 0 | 2 | 84.6% | 63% |
| | *17/*17 | 13 | 12 | 0 | 1 | 92.3% | 72% |
| | *2/*3 | 13 | 8 | 0 | 5 | 61.5% | 40% |
| | *2/*17 | 13 | 13 | 0 | 0 | 100.0% | 83% |
| | Total | 52 | 44 | 0 | 8 | 84.6% | 75% |
| 2 pooled swabs | *1/*1 | 13 | 13 | 0 | 0 | 100.0% | 83% |
| | *17/*17 | 13 | 13 | 0 | 0 | 100.0% | 83% |
| | *2/*3 | 13 | 13 | 0 | 0 | 100.0% | 83% |
| | *2/*17 | 13 | 13 | 0 | 0 | 100.0% | 83% |
| | Total | 52 | 52 | 0 | 0 | 100.0% | 95% |
| Normal Swab | *1/*1 | 13 | 13 | 0 | 0 | 100.0% | 83% |
| | *17/*17 | 13 | 13 | 0 | 0 | 100.0% | 83% |
| | *2/*3 | 13 | 12 | 0 | 1 | 92.3% | 72% |
| | *2/*17 | 13 | 13 | 0 | 0 | 100.0% | 83% |
| | Total | 52 | 51 | 0 | 1 | 98.1% | 92% |
| 1 Half Stroke | *1/*1 | 13 | 12 | 0 | 1 | 92.3% | 72% |
| | *17/*17 | 13 | 13 | 0 | 0 | 100.0% | 83% |
| | *2/*3 | 13 | 13 | 0 | 0 | 100.0% | 83% |
| | *2/*17 | 13 | 13 | 0 | 0 | 100.0% | 83% |
| | Total | 52 | 51 | 0 | 1 | 98.1% | 92% |
| Inside Mouth Touch | *1/*1 | 13 | 10 | 0 | 3 | 76.9% | 54% |
| | *17/*17 | 13 | 12 | 0 | 1 | 92.3% | 72% |
| | *2/*3 | 13 | 9 | 0 | 4 | 69.2% | 46% |
| | *2/*17 | 13 | 13 | 0 | 0 | 100.0% | 83% |
| | Total | 52 | 44 | 0 | 8[c] | 84.6% | 75% |

[a] Genotyped by bi-directional sequencing; *1/*1 samples are wild-type for *2, *3, and *17.
[b] In order for a sample to be deemed a correct call, results of all three genotypes (*2, *3, *17) had to be correct.
[c] Collection of sub-optimal amounts of buccal material results in an increased rate of No calls and Internal Control Errors.

| Test Condition | Genotype[a] | # Samples tested | # Correct calls[b] | # Incorrect calls | # No calls | % Correct calls | 95% One-sided confidence lower limit) |
|---|---|---|---|---|---|---|---|
| 5 pooled swabs | *1/*1 | 13 | 12 | 0 | 1 | 92.3% | 72% |
| | *17/*17 | 13 | 13 | 0 | 0 | 100.0% | 83% |
| | *2/*3 | 13 | 13 | 0 | 0 | 100.0% | 83% |
| | *2/*17 | 13 | 13 | 0 | 0 | 100.0% | 83% |
| | Total | 52 | 51 | 0 | 1 | 98.1% | 92% |
| 2 pooled swabs | *1/*1 | 13 | 13 | 0 | 0 | 100.0% | 83% |
| | *17/*17 | 13 | 13 | 0 | 0 | 100.0% | 83% |
| | *2/*3 | 13 | 13 | 0 | 0 | 100.0% | 83% |
| | *2/*17 | 13 | 13 | 0 | 0 | 100.0% | 83% |
| | Total | 52 | 52 | 0 | 0 | 100.0% | 95% |
| Normal Swab | *1/*1 | 13 | 13 | 0 | 0 | 100.0% | 83% |
| | *17/*17 | 13 | 13 | 0 | 0 | 100.0% | 83% |
| | *2/*3 | 13 | 13 | 0 | 0 | 100.0% | 83% |
| | *2/*17 | 13 | 13 | 0 | 0 | 100.0% | 83% |
| | Total | 52 | 52 | 0 | 0 | 100.0% | 95% |
| 1 Half Stroke | *1/*1 | 13 | 13 | 0 | 0 | 100.0% | 83% |
| | *17/*17 | 13 | 13 | 0 | 0 | 100.0% | 83% |
| | *2/*3 | 13 | 13 | 0 | 0 | 100.0% | 83% |
| | *2/*17 | 13 | 13 | 0 | 0 | 100.0% | 83% |
| | Total | 52 | 52 | 0 | 0 | 100.0% | 95% |
| Inside Mouth Touch | *1/*1 | 13 | 13 | 0 | 0 | 100.0% | 83% |
| | *17/*17 | 13 | 13 | 0 | 0 | 100.0% | 83% |
| | *2/*3 | 13 | 13 | 0 | 0 | 100.0% | 83% |
| | *2/*17 | 13 | 13 | 0 | 0 | 100.0% | 83% |
| | Total | 52 | 52 | 0 | 0 | 100.0% | 95% |

[a] Genotype by bi-directional sequencing; *1/*1 samples are wild-type for *2, *3, and *17.
[b] In order for a sample to be deemed a correct call, results of all three genotypes (*2, *3, *17) had to be correct.

The first pass correct call rate at input levels lower than 0.1 swabs per test was 84.6%. Therefore, the lower limit of detection of the Spartan RX CYP2C19 System is **0.1 swabs per test**.

Table 2b

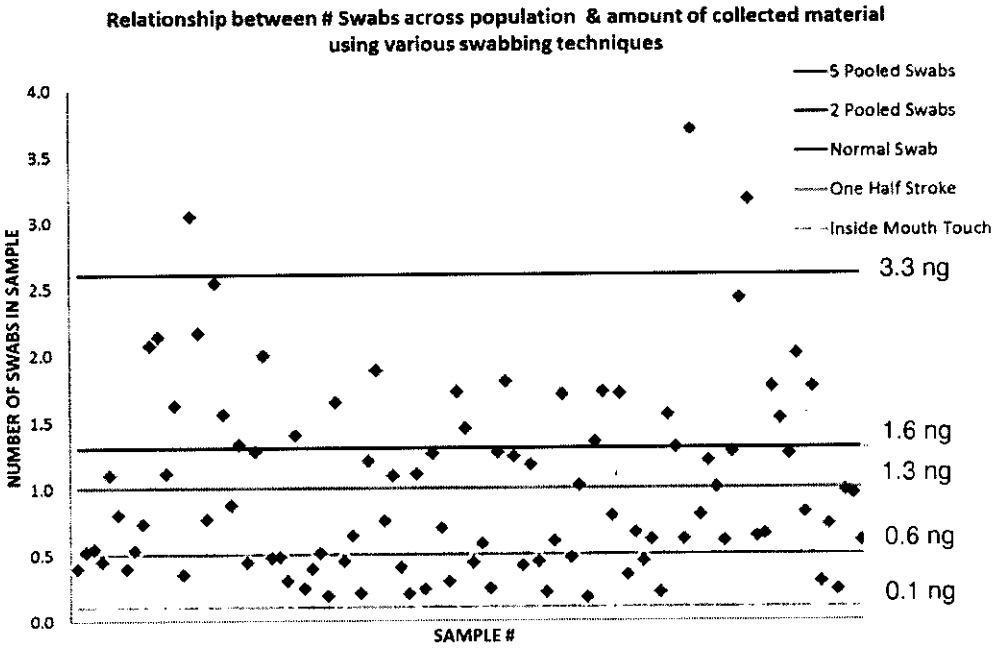


**Figure 1 – Relationship between the normal swab population & the amount of material collected using the various swabbing techniques as outlined in the protocol.** The corresponding average amount of genomic DNA (ng) collected using each swabbing technique is indicated on the right side of the graph.

These experiments indicate that there are two consequences when excessively high or low amounts of buccal material are collected. Either the system generates an internal control abort (Positive System Control fail) or the system generates a No call result. To avoid these consequences, the Instructions for Use recommend that operators swab firmly with 3x up-and-down strokes. Based on these results, proper swabbing is an important factor that influences the rate of No call results. Also, the results from Part 3 demonstrated the system's lower limit of detection when using genomic DNA. The recommended quantity of DNA for external controls was based on these results.

***Method Comparison***

The Spartan RX CYP2C19 System was compared to bi-directional sequencing. Samples were de-identified to protect patient identity. Genomic DNA was extracted from saliva samples. If the result of the first test for a particular individual was a No call, the test was repeated (second pass).

The Method Comparison study was performed by 10 operators at three different locations. The operators had no previous swabbing experience. Of the 327 samples tested, sequencing was unsuccessful for 2 samples—these samples were excluded from the analysis. Of the 325 samples included in the analysis, 4 samples gave a No call result on the first pass test and were re-tested. After the second pass, all samples were called correctly. No samples were called incorrectly. The overall correct call rate for the first pass and second pass tests was 98.8% and 100%, respectively.

For this study, 1/3 of samples collected were tested immediately (4 minutes pre-swabbing and 8 minutes post-swabbing); 1/3 were tested after 10 minutes (4 minutes pre-swabbing and 10 minutes post-swabbing); and 1/3 were tested after 60 minutes (45 minutes pre-swabbing and 60 minutes post swabbing) of storage in the Sample Transport System after swab insertion.

Results of first and second pass tests are summarized in Tables 3a and 3b, respectively.

| Genotype[a] | # Samples tested | # Correct Calls[b] | # Incorrect calls | # No calls | % Correct calls | 95% One-sided confidence lower limit |
|---|---|---|---|---|---|---|
| *1/*1 | 130 | 128 | 0 | 2 | 98.5% | 95% |
| *1/*2 | 95 | 94 | 0 | 1 | 98.9% | 95% |
| *2/*2 | 19 | 19 | 0 | 0 | 100.0% | 88% |
| *1/*3 | 7 | 7 | 0 | 0 | 100.0% | 72% |
| *3/*3 | 1 | 1 | 0 | 0 | 100.0% | 27% |
| *1/*17 | 40 | 39 | 0 | 1 | 97.5% | 90% |
| *17/*17 | 11 | 11 | 0 | 0 | 100.0% | 80% |
| *2/*3 | 6 | 6 | 0 | 0 | 100.0% | 69% |
| *2/*17 | 15 | 15 | 0 | 0 | 100.0% | 85% |
| *3/*17 | 1 | 1 | 0 | 0 | 100.0% | 27% |
| TOTAL | 325 | 321 | 0 | 4 | 98.8% | 97% |

[a] Genotype by bi-directional sequencing; *1/*1 samples are wild-type for *2, *3, and *17.
[b] In order for a sample to be deemed a correct call, results of all three genotypes (*2, *3, *17) had to be correct.

**Table 3b – Method Comparison – SECOND PASS**

| Genotype[a] | # Samples tested | # Correct Calls[b] | # Incorrect calls | # No calls | % Correct calls | 95% One-sided confidence lower limit |
|---|---|---|---|---|---|---|
| *1/*1 | 130 | 130 | 0 | 0 | 100.0% | 98% |
| *1/*2 | 95 | 95 | 0 | 0 | 100.0% | 97% |
| *2/*2 | 19 | 19 | 0 | 0 | 100.0% | 88% |
| *1/*3 | 7 | 7 | 0 | 0 | 100.0% | 72% |
| *3/*3 | 1 | 1 | 0 | 0 | 100.0% | 27% |
| *1/*17 | 40 | 40 | 0 | 0 | 100.0% | 94% |
| *17/*17 | 11 | 11 | 0 | 0 | 100.0% | 80% |
| *2/*3 | 6 | 6 | 0 | 0 | 100.0% | 69% |
| *2/*17 | 15 | 15 | 0 | 0 | 100.0% | 85% |
| *3/*17 | 1 | 1 | 0 | 0 | 100.0% | 27% |
| TOTAL | 325 | 325 | 0 | 0 | 100.0% | 99% |

[a] Genotype by bi-directional sequencing; *1/*1 samples are wild-type for *2, *3, and *17.
[b] In order for a sample to be deemed a correct call, results of all three genotypes (*2, *3, *17) had to be correct.

For the Transport System, the first pass results were 109/110, 105/106,107/109 for the immediate, 10 minute and 60 minute time points, respectively. All results were 100% on the second pass.

**Table 4 – Inter-Laboratory Reproducibility – FIRST PASS**

Buccal swab samples were collected from *1/*17, *2/*3, *1/*1, *17/*17, *1/*3, *2/*17, *2/*2, and *1/*2 individuals (one individual per genotype) across three sites. Genotypes of the eight individuals were confirmed by bi-directional sequencing. Two operators were employed at each site, and tests were performed across five non-consecutive days. Typically, operators were laboratory technicians who had no previous experience with swabbing. At one site, two of the operators did not work in the medical or laboratory field. There were two sessions per day (AM and PM), and each session was split into two sub-sessions. In each sub-session, each of the eight individuals was tested once by Operator 1 and once by Operator 2. If the result of the first test for a particular individual was a No call, the test was repeated (second pass). Results of the inter-laboratory reproducibility study are presented in Tables 4a and 4b.

**Table 4a – Inter-Laboratory Reproducibility – FIRST PASS**

| Sample Type[a] | Site | # samples tested | # no calls | # incorrect calls | # correct calls[b] | % correct call rate | 95% Confidence Limit |
|---|---|---|---|---|---|---|---|
| *1/*1 | 1 | 40 | 0 | 0 | 40 | 100.0% | 94% |
| | 3 | 40 | 1 | 0 | 39 | 97.5% | 90% |
| | 4 | 40 | 0 | 1* | 39 | 97.5% | 90% |
| | Total | 120 | 1 | 1 | 118 | 98.3% | 95% |
| *1/*2 | 1 | 40 | 0 | 0 | 40 | 100.0% | 94% |
| | 3 | 40 | 0 | 0 | 40 | 100.0% | 94% |
| | 4 | 40 | 0 | 0 | 40 | 100.0% | 94% |
| | Total | 120 | 0 | 0 | 120 | 100.0% | 98% |
| *2/*2 | 1 | 40 | 2 | 0 | 38 | 95.0% | 86% |
| | 3 | 40 | 0 | 0 | 40 | 100.0% | 94% |
| | 4 | 40 | 0 | 0 | 40 | 100.0% | 94% |
| | Total | 120 | 2 | 0 | 118 | 98.3% | 95% |
| *1/*3 | 1 | 40 | 1 | 0 | 39 | 97.5% | 90% |
| | 3 | 40 | 1 | 0 | 39 | 97.5% | 90% |
| | 4 | 40 | 0 | 0 | 40 | 100.0% | 94% |
| | Total | 120 | 2 | 0 | 118 | 98.3% | 95% |
| *2/*3 | 1 | 40 | 0 | 0 | 40 | 100.0% | 94% |
| | 3 | 40 | 0 | 0 | 40 | 100.0% | 94% |
| | 4 | 40 | 3 | 0 | 37 | 92.5% | 83% |
| | Total | 120 | 3 | 0 | 117 | 97.5% | 94% |
| *1/*17 | 1 | 40 | 0 | 0 | 40 | 100.0% | 94% |
| | 3 | 40 | 0 | 0 | 40 | 100.0% | 94% |
| | 4 | 40 | 0 | 0 | 40 | 100.0% | 94% |
| | Total | 120 | 0 | 0 | 120 | 100.0% | 98% |
| *17/*17 | 1 | 40 | 0 | 0 | 40 | 100.0% | 94% |
| | 3 | 40 | 1 | 0 | 39 | 97.5% | 90% |
| | 4 | 40 | 1 | 0 | 39 | 97.5% | 90% |
| | Total | 120 | 2 | 0 | 118 | 98.3% | 95% |
| *2/*17 | 1 | 40 | 0 | 0 | 40 | 100.0% | 94% |
| | 3 | 40 | 0 | 0 | 40 | 100.0% | 94% |
| | 4 | 40 | 0 | 0 | 40 | 100.0% | 94% |
| | Total | 120 | 0 | 0 | 120 | 100.0% | 98% |
| TOTAL | 1 | 320 | 3 | 0 | 317 | 99.1% | 98% |
| | 3 | 320 | 3 | 0 | 317 | 99.1% | 98% |
| | 4 | 320 | 4 | 1 | 315 | 98.4% | 97% |
| | Total | 960 | 10 | 1 | 949 | 98.9% | 98% |

[a] Genotype by bi-directional sequencing; *1/*1 samples are wild-type for *2, *3, and *17.

[b] In order for a sample to be deemed a correct call, results of all three genotypes (*2, *3, *17) had to be correct.

*The root cause of the incorrect call could not conclusively be determined, but it was not due to bubbles in the reaction tube.

| Sample Type[a] | Site | # samples tested | # no calls | # incorrect calls | # correct calls[b] | % correct call rate | 95% Confidence Limit |
|---|---|---|---|---|---|---|---|
| *1/*1 | 1 | 40 | 0 | 0 | 40 | 100.0% | 94% |
| | 3 | 40 | 0 | 0 | 40 | 100.0% | 94% |
| | 4 | 40 | 0 | 1* | 39 | 97.5% | 90% |
| | Total | 120 | 0 | 1 | 119 | 99.2% | 96% |
| *1/*2 | 1 | 40 | 0 | 0 | 40 | 100.0% | 94% |
| | 3 | 40 | 0 | 0 | 40 | 100.0% | 94% |
| | 4 | 40 | 0 | 0 | 40 | 100.0% | 94% |
| | Total | 120 | 0 | 0 | 120 | 100.0% | 98% |
| *2/*2 | 1 | 40 | 0 | 0 | 40 | 100.0% | 94% |
| | 3 | 40 | 0 | 0 | 40 | 100.0% | 94% |
| | 4 | 40 | 0 | 0 | 40 | 100.0% | 94% |
| | Total | 120 | 0 | 0 | 120 | 100.0% | 98% |
| *1/*3 | 1 | 40 | 0 | 0 | 40 | 100.0% | 94% |
| | 3 | 40 | 0 | 0 | 40 | 100.0% | 94% |
| | 4 | 40 | 0 | 0 | 40 | 100.0% | 94% |
| | Total | 120 | 0 | 0 | 120 | 100.0% | 98% |
| *2/*3 | 1 | 40 | 0 | 0 | 40 | 100.0% | 94% |
| | 3 | 40 | 0 | 0 | 40 | 100.0% | 94% |
| | 4 | 40 | 1 | 0 | 39 | 97.5% | 90% |
| | Total | 120 | 1 | 0 | 119 | 99.2% | 96% |
| *1/*17 | 1 | 40 | 0 | 0 | 40 | 100.0% | 94% |
| | 3 | 40 | 0 | 0 | 40 | 100.0% | 94% |
| | 4 | 40 | 0 | 0 | 40 | 100.0% | 94% |
| | Total | 120 | 0 | 0 | 120 | 100.0% | 98% |
| *17/*17 | 1 | 40 | 0 | 0 | 40 | 100.0% | 94% |
| | 3 | 40 | 0 | 0 | 40 | 100.0% | 94% |
| | 4 | 40 | 0 | 0 | 40 | 100.0% | 94% |
| | Total | 120 | 0 | 0 | 120 | 100.0% | 98% |
| *2/*17 | 1 | 40 | 0 | 0 | 40 | 100.0% | 94% |
| | 3 | 40 | 0 | 0 | 40 | 100.0% | 94% |
| | 4 | 40 | 0 | 0 | 40 | 100.0% | 94% |
| | Total | 120 | 0 | 0 | 120 | 100.0% | 98% |
| TOTAL | 1 | 320 | 0 | 0 | 320 | 100.0% | 99% |
| | 3 | 320 | 0 | 0 | 320 | 100.0% | 99% |
| | 4 | 320 | 1 | 1 | 318 | 99.4% | 99% |
| | Total | 960 | 1 | 1 | 958 | 99.8% | 99% |

[a] Genotype by bi-directional sequencing; *1/*1 samples are wild-type for *2, *3, and *17.
[b] In order for a sample to be deemed a correct call, results of all three genotypes (*2, *3, *17) had to be correct.
*The root cause of the incorrect call could not conclusively be determined, but it was not due to bubbles in the reaction tube.

Overall, a total of 960 tests were performed—10 second pass tests were performed due to No calls on the first pass test, and all but 1 were recovered.

Overall, after second pass testing of No call genotype results, the Spartan RX CYP2C19 System produced a correct call rate of 99.8%, with a 95% one-sided lower confidence limit of 99%.

### Reagent Lot-to-Lot Reproducibility – SECOND PASS

Lot-to-lot reproducibility was assessed using three independent lots of each reagent type labeled as 1,2 and 3 and performed concurrently with the Site 1 Inter-laboratory Reproducibility study.

On the first pass, 3 samples produced No call results. After the second pass, all of these samples produced correct results. Overall, the results indicate that different reagent lots perform equivalently.

First and second pass results for the Reagent Lot-to-Lot Reproducibility study are presented in Tables 5a and 5b, respectively.

**Table 5a – Reagent Lot-to-Lot Reproducibility – FIRST PASS**

| Reagent Lot | Genotype[a] | # Samples tested | # Correct calls[b] | # incorrect calls | # No calls | % Correct calls (95% one-sided confidence lower limit) |
|---|---|---|---|---|---|---|
| Lot 1 | *2/*17 | 13 | 13 | 0 | 0 | 100% (83%) |
| | *1/*2 | 14 | 14 | 0 | 0 | 100% (84%) |
| | *1/*17 | 13 | 13 | 0 | 0 | 100% (83%) |
| | *17/*17 | 13 | 13 | 0 | 0 | 100% (83%) |
| | *1/*1 | 14 | 14 | 0 | 0 | 100% (84%) |
| | *2/*3 | 13 | 13 | 0 | 0 | 100% (83%) |
| | *2/*2 | 13 | 11 | 0 | 2 | 85% (63%) |
| | *1/*3 | 14 | 13 | 0 | 1 | 93% (73%) |
| | Total | 107 | 104 | 0 | 3 | 97% (93%) |
| Lot 2 | *2/*17 | 13 | 13 | 0 | 0 | 100% (83%) |
| | *1/*2 | 13 | 13 | 0 | 0 | 100% (83%) |
| | *1/*17 | 14 | 14 | 0 | 0 | 100% (84%) |
| | *17/*17 | 13 | 13 | 0 | 0 | 100% (83%) |
| | *1/*1 | 13 | 13 | 0 | 0 | 100% (83%) |
| | *2/*3 | 14 | 14 | 0 | 0 | 100% (84%) |
| | *2/*2 | 13 | 13 | 0 | 0 | 100% (83%) |
| | *1/*3 | 13 | 13 | 0 | 0 | 100% (83%) |
| | Total | 106 | 106 | 0 | 0 | 100% (98%) |
| Lot 3 | *2/*17 | 14 | 14 | 0 | 0 | 100% (84%) |
| | *1/*2 | 13 | 13 | 0 | 0 | 100% (83%) |
| | *1/*17 | 13 | 13 | 0 | 0 | 100% (83%) |
| | *17/*17 | 14 | 14 | 0 | 0 | 100% (84%) |
| | *1/*1 | 13 | 13 | 0 | 0 | 100% (83%) |
| | *2/*3 | 13 | 13 | 0 | 0 | 100% (83%) |
| | *2/*2 | 14 | 14 | 0 | 0 | 100% (84%) |
| | *1/*3 | 13 | 13 | 0 | 0 | 100% (83%) |
| | Total | 107 | 107 | 0 | 0 | 100% (98%) |

[a] Genotype by bi-directional sequencing; *1/*1 samples are wild-type for *2, *3, and *17.
[b] In order for a sample to be deemed a correct call, results of all three genotypes (*2, *3, *17) had to be correct.

**Table 5b – Reagent Lot-to-Lot Reproducibility – SECOND PASS**

| Reagent Lot | Genotype[a] | # Samples tested | # Correct calls[b] | # incorrect calls | # No calls | % Correct calls (95% one-sided confidence lower limit) |
|---|---|---|---|---|---|---|
| Lot 1 | *2/*17 | 13 | 13 | 0 | 0 | 100% (83%) |
| | *1/*2 | 14 | 14 | 0 | 0 | 100% (84%) |
| | *1/*17 | 13 | 13 | 0 | 0 | 100% (83%) |
| | *17/*17 | 13 | 13 | 0 | 0 | 100% (83%) |
| | *1/*1 | 14 | 14 | 0 | 0 | 100% (84%) |
| | *2/*3 | 13 | 13 | 0 | 0 | 100% (83%) |
| | *2/*2 | 13 | 13 | 0 | 0 | 100% (83%) |
| | *1/*3 | 14 | 14 | 0 | 0 | 100% (84%) |
| | Total | 107 | 107 | 0 | 0 | 100% (98%) |
| Lot 2 | *2/*17 | 13 | 13 | 0 | 0 | 100% (83%) |
| | *1/*2 | 13 | 13 | 0 | 0 | 100% (83%) |
| | *1/*17 | 14 | 14 | 0 | 0 | 100% (84%) |
| | *17/*17 | 13 | 13 | 0 | 0 | 100% (83%) |
| | *1/*1 | 13 | 13 | 0 | 0 | 100% (83%) |
| | *2/*3 | 14 | 14 | 0 | 0 | 100% (84%) |
| | *2/*2 | 13 | 13 | 0 | 0 | 100% (83%) |
| | *1/*3 | 13 | 13 | 0 | 0 | 100% (83%) |
| | Total | 106 | 106 | 0 | 0 | 100% (98%) |
| Lot 3 | *2/*17 | 14 | 14 | 0 | 0 | 100% (84%) |
| | *1/*2 | 13 | 13 | 0 | 0 | 100% (83%) |
| | *1/*17 | 13 | 13 | 0 | 0 | 100% (83%) |
| | *17/*17 | 14 | 14 | 0 | 0 | 100% (84%) |
| | *1/*1 | 13 | 13 | 0 | 0 | 100% (83%) |
| | *2/*3 | 13 | 13 | 0 | 0 | 100% (83%) |
| | *2/*2 | 14 | 14 | 0 | 0 | 100% (84%) |
| | *1/*3 | 13 | 13 | 0 | 0 | 100% (83%) |
| | Total | 107 | 107 | 0 | 0 | 100% (98%) |

[a] Genotype by bi-directional sequencing; *1/*1 samples are wild-type for *2, *3, and *17.
[b] In order for a sample to be deemed a correct call, results of all three genotypes (*2, *3, *17) had to be correct.

**Exogenous and Endogenous Interfering Substances**

Interference from exogenous and endogenous interfering substances was evaluated using buccal swab samples collected from *1/*1, *2/*17, *17/*17, and *2/*3 individuals. Genotypes of all individuals were confirmed by bi-directional sequencing prior to initiation of the study.

To test the impact of exogenous substances, buccal swab samples were collected from individuals after exposure to the substance. The individuals rinsed with water (as per the Instructions for Use for the Spartan RX CYP2C19 System) before swab collection.

Direct exposure of individuals to endogenous substances was not possible. Therefore, these substances were added directly to the reagent tube immediately prior to insertion of the buccal swab sample. Note that the Instructions for Use require the patient to rinse his or her mouth with water prior to collection of the buccal swab sample. The purpose of the water rinse is to remove any contaminating endogenous materials such as blood or blood components. So although certain endogenous substances will interfere with performance of the Spartan RX CYP2C19 System, this risk is mitigated by the water rinse.

The following exogenous and endogenous substances were tested:

- Antiseptic mouthwash - 20 ml – Rinse around mouth for 30 s
- Toothpaste - 3/4" Strip – Brush teeth for 2 min, spit
- Baking soda solution - 30 ml (0.1 g /ml) – Rinse around mouth for 10 s
- Cough syrup - 30 ml – Rinse around mouth for 10 s
- Cranberry juice - 30 ml – Rinse around mouth for 10 s
- Salt water - 30 ml (0.01 g/ml) – Rinse around mouth for 10 s
- Sugar water - 30 ml (0.01 g/ml) – Rinse around mouth for 10 s
- Meat - 15 g – Chew for 10 s
- Chewing gum - 1 standard piece – Chew for 1 min
- Hard candy - 1 standard piece – Suck until fully dissolved
- Tobacco smoking - 1 cigar – 5 puffs
- Denture paste - 3 strips – Apply strips to roof of mouth, leave for 5 min, remove
- Human Oral Bacteria - Approximately $9 \times 10^4$ cells (in addition to normal oral flora)
- Whole Blood - 3.5 µl of 0.5% blood (diluted in saliva)

A total of 16 samples were tested for each exogenous and endogenous interfering substance (n=4 per genotype tested). If the result of the first test for a particular individual was a No call, the test was repeated (second pass).

The results of the Exogenous and Endogenous Interfering Substances study indicate that substances commonly introduced into the oral environment do not affect performance of the Spartan RX CYP2C19 System. Nevertheless, proper rinsing and swabbing techniques must be followed to minimize the rate of No calls associated with inhibiting substances.

Results of first and second pass tests performed during the Exogenous and Endogenous Interfering Substances study are summarized in Tables 6a and 6b, respectively.

| Genotype | Substance | # Samples tested | # Correct calls[a] | # incorrect calls | # No calls | % Correct calls | 95% one-sided confidence lower limit |
|---|---|---|---|---|---|---|---|
| Combined genotype results | Mouthwash | 16 | 15 | 0 | 1 | 93.8% | 76% |
| | Toothpaste | 16 | 5 | 0 | 11 | 31.3% | 16% |
| | Baking soda | 16 | 14 | 0 | 2 | 87.5% | 68% |
| | Cough syrup | 16 | 16 | 0 | 0 | 100.0% | 86% |
| | Cranberry juice | 16 | 16 | 0 | 0 | 100.0% | 86% |
| | NaCl solution | 16 | 16 | 0 | 0 | 100.0% | 86% |
| | Sugar solution | 16 | 16 | 0 | 0 | 100.0% | 86% |
| | Meat (horse) | 16 | 16 | 0 | 0 | 100.0% | 86% |
| | Chewing gum | 16 | 14 | 0 | 2 | 87.5% | 68% |
| | Hard candy | 16 | 16 | 0 | 0 | 100.0% | 86% |
| | Tobacco (cigar) | 16 | 15 | 0 | 1 | 93.8% | 76% |
| | Denture paste | 16 | 16 | 0 | 0 | 100.0% | 86% |
| | Bacteria | 16 | 15 | 0 | 1 | 93.8% | 76% |
| | Whole blood | 16 | 15 | 0 | 1 | 93.8% | 76% |
| | Total | 224 | 205 | 0 | 19 | 91.5% | 88% |

[a] In order for a sample to be deemed a correct call, results of all three genotypes (*2, *3, *17) had to be correct.

**Table 6b – Exogenous and Endogenous Interfering Substances – SECOND PASS**

| Genotype | Substance | # Samples tested | # Correct calls[a] | # incorrect calls | # No calls | % Correct calls | 95% one-sided confidence lower limit |
|---|---|---|---|---|---|---|---|
| Combined genotype results | Mouthwash | 16 | 16 | 0 | 0 | 100.00% | 86% |
| | Toothpaste | 16 | 15 | 0 | 1[b] | 93.75% | 76% |
| | Baking soda | 16 | 16 | 0 | 0 | 100.00% | 86% |
| | Cough syrup | 16 | 16 | 0 | 0 | 100.00% | 86% |
| | Cranberry juice | 16 | 16 | 0 | 0 | 100.00% | 86% |
| | NaCl solution | 16 | 16 | 0 | 0 | 100.00% | 86% |
| | Sugar solution | 16 | 16 | 0 | 0 | 100.00% | 86% |
| | Meat (horse) | 16 | 16 | 0 | 0 | 100.00% | 86% |
| | Chewing gum | 16 | 16 | 0 | 0 | 100.00% | 86% |
| | Hard candy | 16 | 16 | 0 | 0 | 100.00% | 86% |
| | Tobacco (cigar) | 16 | 16 | 0 | 0 | 100.00% | 86% |
| | Denture paste | 16 | 16 | 0 | 0 | 100.00% | 86% |
| | Bacteria | 16 | 16 | 0 | 0 | 100.00% | 86% |
| | Whole blood | 16 | 16 | 0 | 0 | 100.00% | 86% |
| | Total | 224 | 223 | 0 | 1 | 99.55% | 98% |

[a] In order for a sample to be deemed a correct call, results of all three genotypes (*2, *3, *17) had to be correct.

[b] First and second pass results for toothpaste were significantly different. For the first pass, three individuals did not rinse out all of the toothpaste before swabbing. For the second pass, all four individuals rinsed out all of the toothpaste and also waited three minutes before swabbing. The results indicate that No calls may be minimized by thoroughly rinsing after brushing, and waiting at least three minutes before swabbing.

DEPARTMENT OF HEALTH & HUMAN SERVICES

Public Health Service

Food and Drug Administration
10903 New Hampshire Avenue
Document Control Center – WO66-G609
Silver Spring, MD 20993-0002

August 12, 2013

Spartan Bioscience Inc.
c/o Lorry Huffman
c/o Myraqua, Inc.
3 Lagoon Drive, Ste 280
REDWOOD SHORES CA 94065

Re: K123891
Trade/Device Name: Spartan RX™ CYP2C19 System
Regulation Number: 21 CFR 862.3360
Regulation Name: Drug metabolizing enzyme genotyping system
Regulatory Class: II
Product Code: NTI, NSU
Dated: June 28, 2013
Received: July 3, 2013

Dear Ms. Huffman:

We have reviewed your Section 510(k) premarket notification of intent to market the device referenced above and have determined the device is substantially equivalent (for the indications for use stated in the enclosure) to legally marketed predicate devices marketed in interstate commerce prior to May 28, 1976, the enactment date of the Medical Device Amendments, or to devices that have been reclassified in accordance with the provisions of the Federal Food, Drug, and Cosmetic Act (Act) that do not require approval of a premarket approval application (PMA). You may, therefore, market the device, subject to the general controls provisions of the Act. The general controls provisions of the Act include requirements for annual registration, listing of devices, good manufacturing practice, labeling, and prohibitions against misbranding and adulteration. Please note: CDRH does not evaluate information related to contract liability warranties. We remind you, however, that device labeling must be truthful and not misleading.

If your device is classified (see above) into either class II (Special Controls) or class III (PMA), it may be subject to additional controls. Existing major regulations affecting your device can be found in the Code of Federal Regulations, Title 21, Parts 800 to 898. In addition, FDA may publish further announcements concerning your device in the Federal Register.

Please be advised that FDA's issuance of a substantial equivalence determination does not mean that FDA has made a determination that your device complies with other requirements of the Act or any Federal statutes and regulations administered by other Federal agencies. You must comply with all the Act's requirements, including, but not limited to: registration and listing (21 CFR Part 807); labeling (21 CFR Part 801); medical device reporting (reporting of medical device-related adverse events) (21 CFR 803); good manufacturing practice requirements as set forth in the quality systems (QS) regulation (21 CFR Part 820); and if applicable, the electronic product radiation control provisions (Sections 531-542 of the Act); 21 CFR 1000-1050.

If you desire specific advice for your device on our labeling regulation (21 CFR Part 801), please go to http://www.fda.gov/AboutFDA/CentersOffices/CDRH/CDRHOffices/ucm115809.htm for the Center for Devices and Radiological Health's (CDRH's) Office of Compliance. Also, please note the regulation entitled, "Misbranding by reference to premarket notification" (21CFR Part 807.97). For questions regarding the reporting of adverse events under the MDR regulation (21 CFR Part 803), please go to http://www.fda.gov/MedicalDevices/Safety/ReportaProblem/default.htm for the CDRH's Office of Surveillance and Biometrics/Division of Postmarket Surveillance.

You may obtain other general information on your responsibilities under the Act from the Division of Small Manufacturers, International and Consumer Assistance at its toll-free number (800) 638-2041 or (301) 796-7100 or at its Internet address http://www.fda.gov/MedicalDevices/ResourcesforYou/Industry/default.htm.

Sincerely yours,

Carol C. Benson -S for

Courtney H. Lias, Ph.D.
Director
Division of Chemistry and Toxicology Devices
Office of In Vitro Diagnostics
and Radiological Health
Center for Devices and Radiological Health

Enclosure

# Indications for Use Form

510(k) Number (if known): K123891

Device Name: Spartan RX CYP2C19 System

Indications for Use:

**Assay -** The Spartan RX CYP2C19 System is indicated for use as an aid to clinicians in determining therapeutic strategies for therapeutics that are metabolized by the Cytochrome P450 2C19 gene product, and that are specifically affected by the *2, *3, and *17 alleles. The Spartan RX CYP2C19 Assay will be run on the Spartan RX Platform from the buccal sample collected with a buccal swab. The Spartan RX CYP2C19 Assay is not indicated to be used to predict drug response or non-response.

**Platform -** The Spartan RX CYP2C19 System is indicated for use as an aid to clinicians in determining therapeutic strategies for therapeutics that are metabolized by the Cytochrome P450 2C19 gene product, and that are specifically affected by the *2, *3, and *17 alleles. The Spartan RX CYP2C19 Platform will be used to run the Spartan RX CYP2C19 Assay.

Prescription Use X (Part 21 CFR 801 Subpart D) AND/OR Over-The-Counter Use _____ (21 CFR 801 Subpart C)

(PLEASE DO NOT WRITE BELOW THIS LINE-CONTINUE ON ANOTHER PAGE OF NEEDED)

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Concurrence of CDRH, Office of In Vitro Diagnostics and Radiological Health (OIR)

Ruth A. Chesler -S

Division Sign-Off
Office of In Vitro Diagnostics and Radiological Health

510(k) k123891